

NA

(1646)

Batch 2-4

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RAW SEQUENCE LISTING

PATENT APPLICATION US/09/418,221

DATE: 02/16/2000
TIME: 11:16:44

Input Set: I418221.RAW

#16

This Raw Listing contains the General Information
Section and up to first 5 pages.

P.S.

ENTERED

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1  <110> APPLICANT: Mahanthappa, Nagesh K.
2  <120> TITLE OF INVENTION: NEUROPROTECTIVE METHODS AND REAGENTS
3  <130> FILE REFERENCE: ONV-043.02
4  <140> CURRENT APPLICATION NUMBER: US/09/418,221
5  <141> CURRENT FILING DATE: 1999-10-14
6  <150> EARLIER APPLICATION NUMBER: 08/883,656
7  <151> EARLIER FILING DATE: 1997-06-27
8  <160> NUMBER OF SEQ ID NOS: 26
9  <170> SOFTWARE: PatentIn Ver. 2.0
10 <210> SEQ ID NO 1
11 <211> LENGTH: 1277
12 <212> TYPE: DNA
13 <213> ORGANISM: chicken Shh
14 <220> FEATURE:
15 <221> NAME/KEY: CDS
16 <222> LOCATION: (1)..(1275)
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20         1             5             10             15
21     tgc gct ctt tta gtc tcc tct ggg ctg act tgt gga cca ggc agg ggc      96
22     Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
23         20             25             30
24     att gga aaa agg agg cac ccc aaa aag ctg acc ccg tta gcc tat aag      144
25     Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
26         35             40             45
27     cag ttt att ccc aat gtg gca gag aag acc cta ggg gcc agt gga aga      192
28     Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
29         50             55             60
30     tat gaa ggg aag atc aca aga aac tcc gag aga ttt aaa gaa cta acc      240
31     Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
32         65             70             75             80
33     cca aat tac aac cct gac att att ttt aag gat gaa gag aac acg gga      288
34     Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
35         85             90             95
36     gct gac aga ctg atg act cag cgc tgc aag gac aag ctg aat gcc ctg      336
37     Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
38         100            105            110
39     gcg atc tcg gtg atg aac cag tgg ccc ggg gtg aag ctg cgg gtg acc      384
40     Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
41         115            120            125
42     gag ggc tgg gac gag gat ggc cat cac tcc gag gaa tcg ctg cac tac      432
43     Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
44         130            135            140

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45	gag ggt cgc gcc gtg gac atc acc acg tcg gat cgg gac cgc agc aag	480
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48	tac gga atg ctg gcc cgc ctc gcc gtc gag gcc ggc ttc gac tgg gtc	528
49	Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
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51	tac tac gag tcc aag gcg cac atc cac tgc tcc gtc aaa gca gaa aac	576
52	Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
53	180 185 190	
54	tca gtg gca gcg aaa tca gga ggc tgc ttc cct ggc tca gcc aca gtg	624
55	Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val	
56	195 200 205	
57	cac ctg gag cat gga ggc acc aag ctg gtg aag gac ctg agc cct ggg	672
58	His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly	
59	210 215 220	
60	gac cgc gtg ctg gct gct gac gcg gac ggc cgg ctg ctc tac agt gac	720
61	Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp	
62	225 230 235 240	
63	ttc ctc acc ttc ctc gac cgg atg gac agc tcc cga aag ctc ttc tac	768
64	Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr	
65	245 250 255	
66	gtc atc gag acg cgg cag ccc cgg gcc cgg ctg cta ctg acg gcg gcc	816
67	Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala	
68	260 265 270	
69	cac ctg ctc ttt gtg gcc ccc cag cac aac cag tcg gag gcc aca ggg	864
70	His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly	
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72	tcc acc agt ggc cag gcg ctc ttc gcc agc aac gtg aag cct ggc caa	912
73	Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln	
74	290 295 300	
75	cgt gtc tat gtg ctg ggc gag ggc ggg cag cag ctg ctg ccg gcg tct	960
76	Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser	
77	305 310 315 320	
78	gtc cac agc gtc tca ttg cgg gag gag gcg tcc gga gcc tac gcc cca	1008
79	Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro	
80	325 330 335	
81	ctc acc gcc cag ggc acc atc ctc atc aac cgg gtg ttg gcc tcc tgc	1056
82	Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys	
83	340 345 350	
84	tac gcc gtc atc gag gag cac agt tgg gcc cat tgg gcc ttc gca cca	1104
85	Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro	
86	355 360 365	
87	ttc cgc ttg gct cag ggg ctg ctg gcc gcc ctc tgc cca gat ggg gcc	1152
88	Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala	
89	370 375 380	
90	atc cct act gcc gcc acc acc acc act ggc atc cat tgg tac tca cgg	1200
91	Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg	
92	385 390 395 400	
93	ctc ctc tac cgc atc ggc agc tgg gtg ctg gat ggt gac gcg ctg cat	1248
94	Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His	

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101     <212> TYPE: DNA
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105     <222> LOCATION: (1)..(1188)
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109      1          5          10          15
110      gca cta tct gcc cag agc tgc ggg ccg ggc cga gga ccg gtt ggc cgg      96
111      Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
112      20          25          30
113      cgg cgt tat gtg cgc aag caa ctt gtg cct ctg cta tac aag cag ttt      144
114      Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
115      35          40          45
116      gtg ccc agt atg ccc gag cgg acc ctg ggc gcg agt ggg cca gcg gag      192
117      Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
118      50          55          60
119      ggg agg gta aca agg ggg tcg gag cgc ttc cgg gac ctc gta ccc aac      240
120      Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
121      65          70          75          80
122      tac aac ccc gac ata atc ttc aag gat gag gag aac agc ggc gca gac      288
123      Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
124      85          90          95
125      cgc ctg atg aca gag cgt tgc aaa gag cgg gtg aac gct cta gcc atc      336
126      Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
127      100          105          110
128      gcg gtg atg aac atg tgg ccc gga gta cgc cta cgt gtg act gaa ggc      384
129      Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
130      115          120          125
131      tgg gac gag gac ggc cac cac gca cag gat tca ctc cac tac gaa ggc      432
132      Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
133      130          135          140
134      cgt gcc ttg gac atc acc acg tct gac cgt gac cgt aat aag tat ggt      480
135      Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
136      145          150          155          160
137      ttg ttg gcg cgc cta gct gtg gaa gcc gga ttc gac tgg gtc tac tac      528
138      Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
139      165          170          175
140      gag tcc cgc aac cac atc cac gta tcg gtc aaa gct gat aac tca ctg      576
141      Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
142      180          185          190
143      gcg gtc cga gcc gga ggc tgc ttt ccg gga aat gcc acg gtg cgc ttg      624
144      Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu

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146	cgg	agc	ggc	gaa	cgg	aag	ggg	ctg	agg	gaa	cta	cat	cgt	ggt	gac	tgg		672	
147	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp			
148		210					215				220								
149	gta	ctg	gcc	gct	gat	gca	gcg	ggc	cga	gtg	gta	ccc	acg	cca	gtg	ctg		720	
150	Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu			
151	225						230				235					240			
152	ctc	ttc	ctg	gac	cgg	gat	ctg	cag	cgc	cgc	gcc	tcg	ttc	gtg	gct	gtg		768	
153	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val			
154					245					250				255					
155	gag	acc	gag	cgg	cct	ccg	cgc	aaa	ctg	ttg	ctc	aca	ccc	tgg	cat	ctg		816	
156	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu			
157				260				265			270								
158	gtg	ttc	gct	gct	cgc	ggg	cca	gcg	cct	gct	cca	ggt	gac	ttt	gca	ccg		864	
159	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro			
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161	gtg	ttc	gcg	cgc	cgc	tta	cgt	gct	ggc	gac	tcg	gtg	ctg	gct	ccc	ggc		912	
162	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly			
163		290					295				300								
164	ggg	gac	gcg	ctc	cag	ccg	gcg	cgc	gta	gcc	cgc	gtg	gcg	cgc	gag	gaa		960	
165	Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu			
166	305					310				315				320					
167	gcc	gtg	ggc	gtg	ttc	gca	ccg	ctc	act	gcg	cac	ggg	acg	ctg	ctg	gtc		1008	
168	Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val			
169				325				330			335								
170	aac	gac	gtc	ctc	gcc	tcc	tgc	tac	gcg	gtt	cta	gag	agt	cac	cag	tgg		1056	
171	Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp			
172			340					345			350								
173	gcc	cac	cgc	gcc	ttc	gcc	cct	ttg	cgg	ctg	ctg	cac	gcg	ctc	ggg	gct		1104	
174	Ala	His	Arg	Ala	Phe	Ala	Pro	Leu	Arg	Leu	Leu	His	Ala	Leu	Gly	Ala			
175		355					360			365									
176	ctg	ctc	cct	ggg	ggt	gca	gtc	cag	ccg	act	ggc	atg	cat	tgg	tac	tct		1152	
177	Leu	Leu	Pro	Gly	Gly	Ala	Val	Gln	Pro	Thr	Gly	Met	His	Trp	Tyr	Ser			
178		370					375			380									
179	cgc	ctc	ctt	tac	cgc	ttg	gcc	gag	gag	tta	atg	ggc	tga					1191	
180	Arg	Leu	Leu	Tyr	Arg	Leu	Ala	Glu	Glu	Leu	Met	Gly							
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191	Met	Ser	Pro	Ala	Trp	Leu	Arg	Pro	Arg	Leu	Arg	Phe	Cys	Leu	Phe	Leu			
192	1					5				10				15					
193	ctg	ctg	ctg	ctt	ctg	gtg	ccg	gcg	gcg	cgg	ggc	tgc	ggg	ccg	ggc	cgg		96	
194	Leu	Leu	Leu	Leu	Leu	Val	Pro	Ala	Ala	Arg	Gly	Cys	Gly	Pro	Gly	Arg			

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I418221.RAW

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1454	W "N" or "Xaa" used: Feature required	Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg A
1458	W "N" or "Xaa" used: Feature required	Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys I
1464	W "N" or "Xaa" used: Feature required	Asp Lys Leu Asn Xaa Leu Ala Ile Ser Val M
1466	W "N" or "Xaa" used: Feature required	Val Xaa Leu Arg Val Thr Glu Gly Trp Asp G
1470	W "N" or "Xaa" used: Feature required	Asp Arg Asp Xaa Ser Lys Tyr Gly Xaa Leu X
1476	W "N" or "Xaa" used: Feature required	Pro Gly Ser Ala Xaa Val Xaa Leu Xaa Xaa G
1478	W "N" or "Xaa" used: Feature required	Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu A
1480	W "N" or "Xaa" used: Feature required	Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe X
1625	W "N" or "Xaa" used: Feature required	Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg A
1627	W "N" or "Xaa" used: Feature required	Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe X
1629	W "N" or "Xaa" used: Feature required	Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu G
1631	W "N" or "Xaa" used: Feature required	Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn T
1633	W "N" or "Xaa" used: Feature required	Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp A
1635	W "N" or "Xaa" used: Feature required	Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile S
1637	W "N" or "Xaa" used: Feature required	Pro Gly Val Xaa Leu Arg Val Thr Glu Gly X
1639	W "N" or "Xaa" used: Feature required	His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly A
1641	W "N" or "Xaa" used: Feature required	Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly X
1643	W "N" or "Xaa" used: Feature required	Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr G
1645	W "N" or "Xaa" used: Feature required	His Xaa Ser Val Lys Xaa Xaa